

Q101072 US-SEQ.txt

SEQUENCE LISTING

<110> UNO, Yukio
HIKICHI, Yukiko
SAGIYA, Yoji
NAKANISHI, Atsushi

<120> Human Sodium-Dependent Bile Acid Transporter Proteins

<130> P04-068US

<140> 10/501,566

<141> 2003-01-16

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Q101072 US-SEQ.txt

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Q101072 US-SEQ.txt

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Q101072 US-SEQ.txt

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Q101072 US-SEQ.txt

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Q101072 US-SEQ.txt

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 Asn Met Leu Tyr Tyr Thr Arg Gly Phe Gln Ser Met Gly Met Tyr Ser
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 Val Tyr Ile Val Phe Leu Leu Gly Phe Gly Val Ala Leu Ala Ser Leu
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Q101072 US-SEQ.txt

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Q101072 US-SEQ.txt

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Q101072 US-SEQ.txt

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 <400> 81
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Q101072 US-SEQ.txt

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Q101072 US-SEQ.txt

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Q101072 US-SEQ.txt

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Q101072 US-SEQ.txt

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Q101072 US-SEQ.txt
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 gaagaagtcg aggaattccc ggaaacctcg gtcg 2373

<210> 104
 <211> 373
 <212> PRT
 <213> Mouse

<400> 104
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 35 40 45
 Phe Gly Cys Ser Val Glu Ser Gln Lys Leu Trp Leu His Leu Arg Arg
 50 55 60
 Pro Trp Gly Ile Ala Val Gly Leu Leu Ser Gln Phe Gly Leu Met Pro
 65 70 75 80
 Leu Thr Ala Tyr Leu Leu Ala Ile Gly Phe Gly Leu Lys Pro Phe Gln
 85 90 95
 Ala Ile Ala Val Leu Met Met Gly Ser Cys Pro Gly Gly Thr Ile Ser
 100 105 110
 Asn Val Leu Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
 115 120 125
 Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
 130 135 140
 Leu Tyr Ile Tyr Thr Arg Ser Trp Thr Leu Thr Gln Asn Leu Val Ile
 145 150 155 160
 Pro Tyr Gln Ser Ile Gly Ile Thr Leu Val Ser Leu Val Val Pro Val
 165 170 175
 Ala Ser Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ala Thr Val
 180 185 190
 Ile Leu Lys Val Gly Ala Ile Leu Gly Gly Met Leu Leu Leu Val Val
 195 200 205
 Ala Val Thr Gly Met Val Leu Ala Lys Gly Trp Asn Thr Asp Val Thr
 210 215 220
 Leu Leu Val Ile Ser Cys Ile Phe Pro Leu Val Gly His Val Thr Gly
 225 230 235 240
 Phe Leu Leu Ala Phe Leu Thr His Gln Ser Trp Gln Arg Cys Arg Thr
 245 250 255
 Ile Ser Ile Glu Thr Gly Ala Gln Asn Ile Gln Leu Cys Ile Ala Met
 260 265 270
 Leu Gln Leu Ser Phe Ser Ala Glu Tyr Leu Val Gln Leu Leu Asn Phe
 275 280 285
 Ala Leu Ala Tyr Gly Leu Phe Gln Val Leu His Gly Leu Leu Ile Val
 290 295 300
 Ala Ala Tyr Gln Ala Tyr Lys Arg Arg Gln Lys Ser Lys Cys Arg Arg
 305 310 315 320
 Gln His Pro Asp Cys Pro Asp Val Cys Tyr Glu Lys Gln Pro Arg Glu
 325 330 335
 Thr Ser Ala Phe Leu Asp Lys Gly Asp Glu Ala Ala Val Thr Leu Gly
 340 345 350
 Pro Val Gln Pro Glu Gln His Arg Ala Ala Glu Leu Thr Ser His
 355 360 365
 Ile Pro Ser Cys Glu
 370

<210> 105
 <211> 1119
 <212> DNA

Q101072 US-SEQ.txt

<213> Mouse

<400> 105

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<211> 24

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<220>

<223> Primer

<400> 106

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<210> 107

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 107

tccttactgg	ccacggagga	ggat	24
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<210> 108

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 108

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<210> 109

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

Q101072 US-SEQ.txt

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<400> 109
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<210> 110
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 110
ccatcatgag gacagcaata g 21

<210> 111
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 111
gagaaggaca gctgcagcat g 21

<210> 112
<211> 1237
<212> DNA
<213> Mouse

<400> 112
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ccgccctgtg gaatggaggg ccatagcgaat ctaaagctgc tttttacagt gctctcggct 180
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agcttgcccc tccatctctc tccgtggcca gtgaaga 1237

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<212> DNA
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<220>
<223> Primer

<400> 113

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cttctg'gcgt ctatgtgaat tatagg

<210> 114
 <211> 19
 <212> DNA
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<220>
 <223> Primer

<400> 114
 gagcatgcca cccagaatg

19

<210> 115
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Probe

<400> 115
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29

<210> 116
 <211> 1046
 <212> DNA
 <213> Rat

<220>
 <221> misc_feature
 <222> (811)..(812)
 <223> a, c, g or t

<400> 116
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 tgggttgatg gagatatgga cctcagcatc agcatgacga cctgctccac agtggctgtc 360
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 ctacccatcc cgtaccagag cataggaatt acccttgggt ccttggtgt tctctgtggc 480
 ccggcatctc tagtgaatta taggtggcca aagcaagcaa cattcattct caaggtcggg 540
 gctgctgttg gcggcatgct cctcctgggt gtggcagtta ccggcgtggt cctggcaaa 600
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 aggaccgctg aactgaccag tcacgt 1046

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<220>
 <223> Primer

<400> 117

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<211> 24		
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<213> Artificial Sequence		
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<223> Primer		
<400> 118		
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<210> 119		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer		
<400> 119		
tccggcatct atgtgaatta tagg		24
<210> 120		
<211> 20		
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<211> 28		
<212> DNA		
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<223> Probe		
<400> 121		
agcaagcaac attcattctc aaggtcgg		28
<210> 122		
<211> 36		
<212> DNA		
<213> Artificial Sequence		
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<223> Primer		
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<210> 123		
<211> 38		
<212> DNA		
<213> Artificial Sequence		
<220>		

<223> Primer

<400> 123
aatgtctaga actagtctat tcacatgaag tgatgtgg 38

<210> 124
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 124
tagaaggcac agtcgagg 18

<210> 125
<211> 317
<212> DNA
<213> Mouse

<400> 125
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gtctgagagg atacaggga tcaagcggct ttctcctgaa gacgtggagt ccatgcggga 180
cattctgaca agaagcatgt accaagtctg acaaagaacc ctatcctaca acaaatacaa 240
ctcctaaacc caacaagtg agaagcaagc caaagagatt ctgatccgtc gccagaacac 300
cttgaggagg agcatgc 317

<210> 126
<211> 23
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<220>
<223> Primer

<400> 126
ccggaggaac ctgccaaaat caa 23

<210> 127
<211> 26
<212> DNA
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<220>
<223> Primer

<400> 127
gcatgctctc cctcaagggtg ttctgg 26

<210> 128
<211> 22
<212> DNA
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<220>
<223> Primer

<400> 128
gatgaaacag gccattgaga tg 22

<210> 129

Q101072 US-SEQ.txt

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<211> 25
<212> DNA
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<220>
<223> Primer

<400> 129
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<210> 130
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<212> DNA
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<220>
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<400> 130
ctgggatact gagctctgtg gctt                24

<210> 131
<211> 363
<212> DNA
<213> Rat

<400> 131
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tgtcttactt agcagccgag acgctttatc tctccggaat cctggccatc acagcttgtg    180
cagtgacaat gaaaaagtac gtggaagaga acgtgtccca gacgtcgtac acgaccatca    240
agtacttcac gaagatgctg agcagcgtga gcgagaccct catcttcac ttcatgggag    300
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tct                                           363

<210> 132
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 132
tcgtgggatg cgggggagta ttt                23

<210> 133
<211> 24
<212> DNA
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<220>
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<400> 133
agaaggccag ggtgaagcag acga                24

<210> 134
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

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<223> Primer
<400> 134
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<212> DNA
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<400> 135
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<211> 25
<212> DNA
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<220>
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<210> 137
<211> 35
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<212> DNA
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<220>
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<213> Artificial Sequence

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<400> 140

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20

<210> 141

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20

<210> 142

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 142

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20

<210> 143

<211> 680

<212> DNA

<213> Mouse

<400> 143

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atactccagt	aaccagcggt	catgccacag	actattttgt	tgttggaat	attgtttaca	420
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<210> 144

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 144

gccatcgac agttttccta cct

23

<210> 145

<211> 24

<212> DNA

Q101072 US-SEQ.txt

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<213> Artificial Sequence

<220>
<223> Primer

<400> 145
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<210> 146
<211> 19
<212> DNA
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<220>
<223> Primer

<400> 146
aaccatctgg ccgaccatc                19

<210> 147
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 147
acgcagagct caggaccata g                21

<210> 148
<211> 24
<212> DNA
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<220>
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<400> 148
tgcctgcctt ttcattgtcag gagc                24

<210> 149
<211> 771
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<400> 149
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attgccacc ttcaactctgg ggatcttcga gaggtcgtgt actcaggaga gcatgctcag    240
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Q101072 US-SEQ.txt

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<213> Artificial Sequence

<220>
<223> Primer

<400> 150
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<210> 151
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 151
accagaagtg ggcagaactc a 21

<210> 152
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 152
catagttgcc tgcctttca tgtcagga 28

<210> 153
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 153
ttggatccgt cgacatgtcc cgggccacgt ctgttgg 37

<210> 154
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 154
ccgcggccgc actagtttat ttcttcttg atttctttt ggt 43

<210> 155
<211> 1064
<212> DNA
<213> Mouse

<400> 155
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gaatgacttc gttaagcgca tgtatgacat gatcctgctg aggagtggca actgggagct 180
ggagaccatg cgcaacaacg atgggctcac gccactgcag ctggctgcc aatggggcaa 240

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tgataaacga	catgagatgc	tgaccctgga	gcctctgcac	acgcgtctac	acacgaaatg 480
gaagaaattt	gccaaagtaca	tgttcttctt	gtccttctgc	ttctattttc	tctacacacat 540
caccttgacc	cttgtctctt	actaccgtcc	tcgggaagat	gaggatctcc	cacacccctt 600
ggccctgaca	cacaaaaatga	gttggttcca	gctcctaggg	aggatgtttg	tcctcatctg 660
ggccacatgc	atctctgtga	aagaaggcat	tgccattttc	ctgctgagac	cctccgatct 720
tcagtccatc	ctgtcagatg	cctgggttca	ctttgtcttt	tttgtccaag	ctgtacttgt 780
gatactgtct	gtattcttgt	actgttttgc	ctacaaagaa	tacctcgctc	gcctcgtgtc 840
ggccatggcc	ctgggctggg	cgaacatgct	ctactacacg	agaggcttcc	agtcctatgg 900
catgtacacg	gtcatgatcc	agaagggtcat	tttgcacgat	gtcctcaagt	tcttgtttgt 960
ttacatctctg	ttcttacttg	gatttggagt	agcgctggcc	tcactgattg	agaagtgtct 1020
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<220>
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<400> 159
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<210> 160
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 <213> Artificial Sequence

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<400> 160
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<210> 161
<211> 34
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<220>
<223> Primer

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34

<210> 162
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<223> Primer

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<220>
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<400> 163
taatacgact cactataggg
20

<210> 164
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<220>
<223> Primer

<400> 164
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24

<210> 165
<211> 23
<212> DNA
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23

<210> 166

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<220>
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<400> 167
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21

<210> 168
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<223> Primer

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<212> DNA
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<400> 169
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21

<210> 170
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24

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<220>
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<400> 171

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ggctctccagc tcccgattgc cac

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<220>
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<400> 172
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<210> 173
 <211> 348
 <212> PRT
 <213> Human

<400> 173

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			20					25					30		
Val	Leu	Ser	Thr	Val	Leu	Thr	Ile	Leu	Ala	Leu	Val	Met	Phe	Ser	
			35				40				45				
Met	Gly	Cys	Asn	Val	Glu	Ile	Lys	Lys	Phe	Leu	Gly	His	Ile	Lys	Arg
			50			55					60				
Pro	Trp	Gly	Ile	Cys	Val	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met	Pro
65					70				75					80	
Leu	Thr	Gly	Phe	Ile	Leu	Ser	Val	Ala	Phe	Asp	Ile	Leu	Pro	Leu	Gln
			85						90				95		
Ala	Val	Val	Val	Leu	Ile	Ile	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Ala	Ser
			100				105						110		
Asn	Ile	Leu	Ala	Tyr	Trp	Val	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val	Ser
			115			120						125			
Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys
			130			135					140				
Leu	Leu	Ile	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Ser	Ile	Val	Ile
145					150				155					160	
Pro	Tyr	Asp	Asn	Ile	Gly	Thr	Ser	Leu	Val	Ala	Leu	Val	Val	Pro	Val
			165						170					175	
Ser	Ile	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys	Ile
			180					185					190		
Ile	Leu	Lys	Ile	Gly	Ser	Ile	Ala	Gly	Ala	Ile	Leu	Ile	Val	Leu	Ile
		195					200					205			
Ala	Val	Val	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Ala	Pro
		210				215					220				
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Val	Ala	Gly	Tyr	Ser	Leu
225					230				235						240
Gly	Phe	Leu	Leu	Ala	Arg	Ile	Ala	Gly	Leu	Pro	Trp	Tyr	Arg	Cys	Arg
			245						250					255	
Thr	Val	Ala	Phe	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr
			260				265						270		
Ile	Val	Gln	Leu	Ser	Phe	Thr	Pro	Glu	Glu	Leu	Asn	Val	Val	Phe	Thr
			275				280					285			
Phe	Pro	Leu	Ile	Tyr	Ser	Ile	Phe	Gln	Leu	Ala	Phe	Ala	Ala	Ile	Phe
			290			295					300				
Leu	Gly	Phe	Tyr	Val	Ala	Tyr	Lys	Lys	Cys	His	Gly	Lys	Asn	Lys	Ala
305					310					315					320
Glu	Ile	Pro	Glu	Ser	Lys	Glu	Asn	Gly	Thr	Glu	Pro	Glu	Ser	Ser	Phe
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Tyr	Lys	Ala	Asn	Gly	Gly	Phe	Gln	Pro	Asp	Glu	Lys				

340

<210> 174
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<212> PRT
<213> Rat

<400> 174

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Ser Ser Ser Pro Thr Gly Gln Gln Thr Pro Asp Ala Arg Phe Ala Ala
35     40     45     50     55     60     65
Ser Ser Ser Asp Pro Asp Glu Arg Ile Ser Val Phe Glu Leu Asp Tyr
50     55     60     65     70     75     80
Asp Tyr Val Gln Ile Pro Tyr Glu Val Thr Leu Trp Ile Leu Leu Ala
65     70     75     80     85     90     95
Ser Leu Ala Lys Ile Gly Phe His Leu Tyr His Arg Leu Pro His Leu
85     90     95     100    105    110    115
Met Pro Glu Ser Cys Leu Leu Ile Ile Val Gly Ala Leu Val Gly Ser
100    105    110    115    120    125    130
Ile Ile Phe Gly Thr His His Lys Ser Pro Pro Val Met Asp Ser Ser
115    120    125    130    135    140    145
Ile Tyr Phe Leu Tyr Leu Leu Pro Pro Ile Val Leu Glu Ser Gly Tyr
130    135    140    145    150    155    160
Phe Met Pro Thr Arg Pro Phe Phe Glu Asn Ile Gly Ser Ile Leu Trp
145    150    155    160    165    170    175
Trp Ala Gly Leu Gly Ala Leu Ile Asn Ala Phe Gly Ile Gly Leu Ser
160    165    170    175    180    185    190
Leu Tyr Phe Ile Cys Gln Ile Lys Ala Phe Gly Leu Gly Asp Ile Asn
175    180    185    190    195    200    205
Leu Leu Gln Asn Leu Leu Phe Gly Ser Leu Ile Ser Ala Val Asp Pro
190    195    200    205    210    215    220
Val Ala Val Leu Ala Val Phe Glu Ala Arg Val Asn Glu Gln Leu
205    210    215    220    225    230    235
Tyr Met Met Ile Phe Gly Glu Ala Leu Leu Asn Asp Gly Ile Ser Val
220    225    230    235    240    245    250
Val Leu Tyr Asn Ile Leu Ile Ala Phe Thr Lys Met His Lys Phe Glu
235    240    245    250    255    260    265
Asp Ile Glu Ala Val Asp Ile Leu Ala Gly Cys Ala Arg Phe Val Ile
250    255    260    265    270    275    280
Val Gly Cys Gly Val Phe Phe Gly Ile Ile Phe Gly Phe Ile Ser
265    270    275    280    285    290    295
Ala Phe Ile Thr Arg Phe Thr Gln Asn Ile Ser Ala Ile Glu Pro Leu
280    285    290    295    300    305    310
Ile Val Phe Met Phe Ser Tyr Leu Ser Tyr Leu Ala Ala Glu Thr Leu
300    305    310    315    320    325    330
Tyr Leu Ser Gly Ile Leu Ala Ile Thr Ala Cys Ala Val Thr Met Lys
310    315    320    325    330    335    340
Lys Tyr Val Glu Asn Val Ser Gln Thr Ser Tyr Thr Thr Ile Lys
325    330    335    340    345    350    355
Tyr Phe Met Lys Met Leu Ser Ser Val Ser Glu Thr Leu Ile Phe Ile
340    345    350    355    360    365    370
Phe Met Gly Val Ser Thr Val Gly Lys Asn His Glu Trp Asn Trp Ala
355    360    365    370    375    380    385
Phe Val Cys Phe Thr Leu Ala Phe Cys Gln Ile Trp Arg Ala Ile Ser
370    375    380    385    390    395    400
Val Phe Thr Leu Phe Tyr Val Ser Asn Gln Phe Arg Thr Phe Pro Phe
385    390    395    400    405    410    415
ser Ile Lys Asp Gln Leu Ile Ile Phe Tyr Ser Gly Val Arg Gly Ala
400    405    410    415    420    425    430

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Lys	Lys	Leu	Phe	Val	Thr	Ala	Thr	Leu	Val	Val	Thr	Tyr	Phe	Thr	Val
		450				455					460				
Phe	Phe	Gln	Gly	Ile	Thr	Ile	Gly	Pro	Leu	Val	Arg	Tyr	Leu	Asp	Val
465					470					475				480	
Arg	Lys	Thr	Asn	Lys	Glu	Ser	Ile	Asn	Glu	Glu	Leu	His	Ile	Arg	
			485					490					495		
Leu	Met	Asp	His	Leu	Lys	Ala	Gly	Ile	Glu	Asp	Val	Cys	Gly	Gln	Trp
			500					505					510		
Ser	His	Tyr	Gln	Val	Arg	Asp	Lys	Phe	Lys	Lys	Phe	Asp	His	Arg	Tyr
		515					520					525			
Leu	Arg	Lys	Ile	Leu	Ile	Arg	Asn	Gln	Pro	Lys	Ser	Ser	Ile	Val	
		530				535					540				
Ser	Lys	Tyr	Lys	Lys	Leu	Glu	Met	Lys	Gln	Ala	Ile	Glu	Met	Ala	Glu
545					550					555				560	
Thr	Gly	Leu	Leu	Ser	Ser	Val	Ala	Ser	Pro	Thr	Pro	Tyr	Gln	Ser	Glu
				565					570					575	
Arg	Ile	Gln	Gly	Ile	Lys	Arg	Leu	Ser	Pro	Glu	Asp	Val	Glu	Ser	Met
			580					585					590		
Arg	Asp	Ile	Leu	Thr	Arg	Asn	Met	Tyr	Gln	Val	Arg	Gln	Arg	Thr	Leu
		595				600						605			
Ser	Tyr	Asn	Lys	Tyr	Asn	Leu	Lys	Pro	Gln	Thr	Ser	Glu	Lys	Gln	Ala
		610				615					620				
Lys	Glu	Ile	Leu	Ile	Arg	Arg	Gln	Asn	Thr	Leu	Arg	Glu	Ser	Leu	Arg
625					630					635				640	
Lys	Gly	Gln	Ser	Leu	Pro	Trp	Val	Lys	Pro	Ala	Gly	Thr	Lys	Asn	Phe
				645					650					655	
Arg	Tyr	Leu	Ser	Phe	Pro	Tyr	Ser	Asn	Pro	Gln	Pro	Ala	Arg	Arg	Gly
			660					665					670		
Ala	Arg	Ala	Ala	Glu	Ser	Thr	Gly	Asn	Pro	Cys	Cys	Trp	Leu	Leu	His
		675					680					685			
Phe	Leu	Leu	Cys	Arg	Ala	Met	Val	Glu	Lys	Ile	Trp	Gly	Pro	Gly	Gly
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 <212> PRT
 <213> Human

<400> 175

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			20				25					30			
Ala	Glu	Thr	Leu	Leu	Asn	Ala	Pro	Arg	Ala	Met	Gly	Thr	Ser	Ser	Ser
		35					40					45			
Pro	Pro	Ser	Pro	Ala	Ser	Val	Val	Ala	Pro	Gly	Thr	Thr	Leu	Phe	Glu
		50				55					60				
Glu	Ser	Arg	Leu	Pro	Val	Phe	Thr	Leu	Asp	Tyr	Pro	His	Val	Gln	Ile
65					70					75				80	
Pro	Phe	Glu	Ile	Thr	Leu	Trp	Ile	Leu	Leu	Ala	Ser	Leu	Ala	Lys	Ile
				85					90						
Gly	Phe	His	Leu	Tyr	His	Lys	Leu	Pro	Thr	Ile	Val	Pro	Glu	Ser	Cys
			100					105					110		
Leu	Leu	Ile	Met	Val	Gly	Leu	Leu	Gly	Gly	Ile	Ile	Phe	Gly	Val	
		115					120					125			
Asp	Glu	Lys	Ser	Pro	Pro	Ala	Met	Lys	Thr	Asp	Val	Phe	Phe	Leu	Tyr
		130				135					140				
Leu	Leu	Pro	Pro	Ile	Val	Leu	Asp	Ala	Gly	Tyr	Phe	Met	Pro	Thr	Arg

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145	Pro	Phe	Phe	Glu	Asn	150	Ile	Gly	Thr	Ile	Phe	155	Trp	Tyr	Ala	Val	160	Val	Gly
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	Gln	Ile	Glu	Ala	Phe		Gly	Leu	Ser	Asp	200	Ile	Thr	Leu	Leu	Gln	Asn	Leu	
	Leu	Phe	Gly	Ser	Leu		Ile	Ser	Ala	Val	215	Asp	Pro	Val	Ala	Val	Leu	Ala	
	Val	Phe	Glu	Asn	Ile		His	Val	Asn	Glu	220	Gln	Tyr	Ile	Leu	Val	Phe	240	
225	Gly	Glu	Ser	Leu	Leu		Asn	Asp	Ala	Val	235	Thr	Val	Val	Leu	Tyr	Asn	Leu	
					245						250						255		
	Phe	Lys	Ser	Phe	Cys		Gln	Met	Lys	Thr	265	Ile	Glu	Thr	Ile	Asp	270	Val	Phe
	Ala	Gly	Ile	Ala	Asn		Phe	Phe	Val	Val	280	Gly	Ile	Gly	Gly	Val	Leu	Ile	
	Gly	Ile	Phe	Leu	Gly		Phe	Ile	Ala	Ala	285	Phe	Thr	Thr	Arg	Phe	Thr	His	
	Asn	Ile	Arg	Val	Ile		Glu	Pro	Leu	Phe	295	Val	Phe	Leu	Tyr	Ser	Tyr	Leu	
305	Ser	Tyr	Ile	Thr	Ala		Glu	Met	Phe	His	310	Leu	Ser	Gly	Ile	Met	Ala	Ile	
					325						330						335		
	Thr	Ala	Cys	Ala	Met		Thr	Met	Asn	Lys	345	Tyr	Val	Glu	Glu	Asn	Val	Ser	
	Gln	Lys	Ser	Tyr	Thr		Thr	Ile	Lys	Tyr	350	Phe	Met	Lys	Met	Leu	Ser	Ser	
	Val	Ser	Glu	Thr	Leu		Ile	Phe	Ile	Phe	360	Met	Gly	Val	Ser	Thr	Val	Gly	
	Lys	Asn	His	Glu	Trp		Asn	Trp	Ala	Phe	375	Val	Cys	Phe	Thr	Leu	Ala	Phe	
385	Cys	Leu	Met	Trp	Arg		Ala	Leu	Gly	Val	390	Phe	Val	Leu	Thr	Gln	Val	Ile	
					405						410						415		
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	Ala	Tyr	Gly	Gly	Leu		Arg	Gly	Ala	Ile	425	Cys	Phe	Ala	Leu	Val	Phe	Leu	
	Leu	Pro	Ala	Ala	Val		Phe	Pro	Arg	Lys	440	Lys	Lys	Leu	Phe	Ile	Thr	Ala	Ala
	Ile	Val	Val	Ile	Phe		Phe	Thr	Val	Phe	455	Ile	Leu	Gly	Ile	Thr	Ile	Arg	
465	Pro	Leu	Val	Glu	Phe		Leu	Asp	Val	Lys	470	Arg	Ser	Asn	Lys	Lys	Gln	Gln	
					485						490						495		
	Ala	Val	Ser	Glu	Glu		Ile	Tyr	Cys	Arg	500	Leu	Phe	Asp	His	Val	Lys	Thr	
	Gly	Ile	Glu	Asp	Val		Cys	Gly	His	Trp	505	Gly	His	Asn	Phe	Trp	Arg	Asp	
	Lys	Phe	Lys	Lys	Phe		Asp	Asp	Lys	Tyr	520	Leu	Arg	Lys	Leu	Leu	Ile	Arg	
	Glu	Asn	Gln	Pro	Lys		Ser	Ser	Ile	Val	535	Ser	Leu	Tyr	Lys	Lys	Leu	Glu	
545	Ile	Lys	His	Ala	Ile		Glu	Met	Ala	Glu	550	Thr	Gly	Met	Ile	Ser	Thr	Val	
					565						570						575		
	Pro	Thr	Phe	Ala	Ser		Leu	Asn	Asp	Cys	585	Arg	Glu	Glu	Lys	Ile	Arg	Lys	
	Val	Thr	Ser	Ser	Glu		Thr	Asp	Glu	Ile	600	Arg	Glu	Leu	Leu	Ser	Arg	Asn	
	Leu	Tyr	Gln	Ile	Arg		Gln	Arg	Thr	Leu	615	Ser	Tyr	Asn	Arg	His	Ser	Leu	
	Thr	Ala	Asp	Thr	Ser		Glu	Arg	Gln	Ala	630	Lys	Glu	Ile	Leu	Ile	Arg	Arg	
625	Arg	His	Ser	Leu	Arg		Glu	Ser	Ile	Arg	635	Lys	Asp	Ser	Ser	Leu	Asn	Arg	
					645						650						655		

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Glu His Arg Ala Ser Thr Ser Thr Ser Arg Tyr Leu Ser Leu Pro Lys
 660 665 670
 Asn Thr Lys Leu Pro Glu Lys Leu Gln Lys Arg Arg Thr Ile Ser Ile
 675 680 685
 Ala Asp Gly Asn Ser Ser Asp Ala Asp Ala Gly Thr Thr Val
 690 695 700
 Leu Asn Leu Gln Pro Arg Ala Arg Phe Leu Pro Glu Gln Phe Ser
 705 710 715 720
 Lys Lys Ser Pro Gln Ser Tyr Lys Met Glu Trp Lys Asn Glu Val Asp
 725 730 735
 Val Asp Ser Gly Arg Asp Met Pro Ser Thr Pro Thr Pro His Ser
 740 745 750
 Arg Glu Lys Gly Thr Gln Thr Ser Gly Leu Leu Gln Gln Leu Leu
 755 760 765
 Ser Lys Asp Gln Ser Gly Ser Glu Arg Glu Asp Ser Thr Glu Gly
 770 775 780
 Ile Pro Pro Lys Pro Pro Arg Leu Val Trp Ala Ser Glu Pro
 785 790 795 800
 Gly Ser Arg Lys Ala Arg Phe Gly Ser Glu Lys Pro
 805 810

<210> 176

<211> 1164

<212> PRT

<213> Human

<400> 176

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 Gln Glu Glu Val Arg Thr Ile Phe Ile Asn Gln Pro Gln Leu Thr Lys
 35 40 45
 Phe Cys Asn Asn His Val Ser Thr Ala Lys Tyr Asn Ile Ile Thr Phe
 50 55 60
 Leu Pro Arg Phe Leu Tyr Ser Gln Phe Arg Arg Ala Ala Asn Ser Phe
 65 70 75 80
 Phe Leu Phe Ile Ala Leu Leu Gln Gln Ile Pro Asp Val Ser Pro Thr
 85 90 95
 Gly Arg Tyr Thr Thr Leu Val Pro Leu Leu Phe Ile Leu Ala Val Ala
 100 105 110
 Ala Ile Lys Glu Ile Ile Glu Asp Ile Lys Arg His Lys Ala Asp Asn
 115 120 125
 Ala Val Asn Lys Lys Gln Thr Gln Val Leu Arg Asn Gly Ala Trp Glu
 130 135 140
 Ile Val His Trp Glu Lys Val Ala Val Gly Glu Ile Val Lys Val Thr
 145 150 155 160
 Asn Gly Glu His Leu Pro Ala Asp Leu Ile Ser Leu Ser Ser Ser Glu
 165 170 175
 Pro Gln Ala Met Cys Tyr Ile Glu Thr Ser Asn Leu Asp Gly Glu Thr
 180 185 190
 Asn Leu Lys Ile Arg Gln Gly Leu Pro Ala Thr Ser Asp Ile Lys Asp
 195 200 205
 Val Asp Ser Leu Met Arg Ile Ser Gly Arg Ile Glu Cys Glu Ser Pro
 210 215 220
 Asn Arg His Leu Tyr Asp Phe Val Gly Asn Ile Arg Leu Asp Gly His
 225 230 235 240
 Gly Thr Val Pro Leu Gly Ala Asp Gln Ile Leu Leu Arg Gly Ala Gln
 245 250 255
 Leu Arg Asn Thr Gln Trp Val His Gly Ile Val Val Tyr Thr Gly His
 260 265 270
 Asp Thr Lys Leu Met Gln Asn Ser Thr Ser Pro Pro Leu Lys Leu Ser

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Asn	Val	275	Glu	Arg	Ile	Thr	Asn	280	Val	Gln	Ile	Leu	Ile	Leu	Phe	Cys	Ile
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Arg	Arg	305	His	Ser	Gly	Lys	Asp	310	Trp	Tyr	Leu	Asn	Leu	Asn	Tyr	Gly	Gly
Ala	Ser	325	Asn	Phe	Gly	Leu	Asn	330	Phe	Leu	Thr	Phe	Ile	Ile	Leu	Phe	Asn
Asn	Leu	340	Ile	Pro	Ile	Ser	Leu	345	Leu	Val	Thr	Leu	Glu	Val	Val	Lys	Phe
Thr	Gln	355	Ala	Tyr	Phe	Ile	Asn	360	Trp	Asp	Leu	Asp	Met	His	Tyr	Glu	Pro
Thr	Asp	370	Thr	Ala	Ala	Met	Ala	375	Arg	Thr	Ser	Asn	Leu	Asn	Glu	Glu	Leu
Gly	Gln	385	Val	Lys	Tyr	Ile	Phe	390	Ser	Asp	Lys	Thr	Gly	Thr	Leu	Thr	Cys
Asn	Val	405	Met	Gln	Phe	Lys	Lys	410	Cys	Thr	Ile	Ala	Gly	Val	Ala	Tyr	Gly
His	Val	420	Pro	Glu	Pro	Glu	Asp	425	Tyr	Gly	Cys	Ser	Pro	Asp	Glu	Trp	Gln
Asn	Ser	435	Gln	Phe	Gly	Asp	Glu	440	Lys	Thr	Phe	Ser	Asp	Ser	Ser	Leu	Leu
Glu	Asn	450	Leu	Gln	Asn	Asn	His	455	Pro	Thr	Ala	Pro	Ile	Ile	Cys	Glu	Phe
Leu	Thr	465	Met	Met	Ala	Val	Cys	470	His	Thr	Ala	Val	Pro	Glu	Arg	Glu	Gly
Asp	Lys	485	Ile	Ile	Tyr	Gln	Ala	490	Ala	Ser	Pro	Asp	Glu	Gly	Ala	Leu	Val
Arg	Ala	500	Lys	Gln	Leu	Asn	Phe	505	Val	Phe	Thr	Gly	Arg	Thr	Pro	Asp	
Ser	Val	515	Ile	Ile	Asp	Ser	Leu	520	Gly	Gln	Glu	Glu	Arg	Tyr	Glu	Leu	Leu
Asn	Val	530	Leu	Glu	Phe	Thr	Ser	535	Ala	Arg	Lys	Arg	Met	Ser	Val	Ile	Val
Arg	Thr	545	Pro	Ser	Gly	Lys	Leu	550	Arg	Leu	Tyr	Cys	Lys	Gly	Ala	Asp	Thr
Val	Ile	565	Tyr	Asp	Arg	Leu	Ala	570	Glu	Thr	Ser	Lys	Tyr	Lys	Glu	Ile	Thr
Leu	Lys	580	His	Leu	Glu	Gln	Phe	585	Glu	Thr	Glu	Gly	Leu	Arg	Thr	Leu	Cys
Phe	Ala	595	Val	Ala	Glu	Ile	Ser	600	Glu	Ser	Asp	Phe	Gln	Glu	Trp	Arg	Ala
Val	Tyr	610	Gln	Arg	Ala	Ser	Thr	615	Ser	Val	Gln	Asn	Arg	Leu	Leu	Lys	Leu
Glu	Glu	625	Ser	Tyr	Glu	Leu	Ile	630	Glu	Lys	Asn	Leu	Gln	Leu	Leu	Gly	Ala
Thr	Ala	645	Ile	Glu	Asp	Lys	Leu	650	Gln	Val	Pro	Glu	Thr	Ile	Glu		
Thr	Leu	660	Met	Lys	Ala	Asp	Ile	665	Lys	Ile	Trp	Ile	Leu	Thr	Gly	Asp	Lys
Gln	Glu	675	Thr	Ala	Ile	Asn	Ile	680	Gly	His	Ser	Cys	Lys	Leu	Lys	Lys	
Asn	Met	690	Gly	Met	Ile	Val	Ile	695	Asn	Glu	Gly	Ser	Leu	Asp	Gly	Thr	Arg
Glu	Thr	705	Leu	Ser	Arg	His	Cys	710	Thr	Thr	Leu	Gly	Asp	Ala	Leu	Arg	Lys
Glu	Asn	725	Asp	Phe	Ala	Leu	Ile	730	Ile	Asp	Gly	Lys	Thr	Leu	Lys	Tyr	Ala
Leu	Thr	740	Phe	Gly	Val	Arg	Gln	745	Phe	Leu	Asp	Leu	Ala	Leu	Ser	Cys	
Lys	Ala	755	Val	Ile	Cys	Cys	Arg	760	Val	Ser	Pro	Leu	Gln	Lys	Ser	Glu	Val
		770						775									

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Val Glu Met Val Lys Lys Gln Val Lys Val Val Thr Leu Ala Ile Gly
 785 Asp Gly Ala Asn Asp 790 Val Ser Met Ile Gln Thr Ala His Val Gly Val
 Gly Ile Ser Gly 805 Asn Glu Gly Leu Gln 810 Ala Asn Ser Ser 815
 Ser Ile Ala 820 Gln Phe Lys Tyr Leu 825 Lys Asn Leu Leu Met 830 Ile His Gly
 Ala Trp 835 Asn Tyr Asn Arg Val 840 Ser Lys Cys Ile Leu Tyr Cys Phe Tyr
 Lys 850 Asn Ile Val Leu Tyr Ile Ile Glu Ile Trp Phe Ala Phe Val Asn
 865 Gly Phe Ser Gly Gln 870 Ile Leu Phe Glu Arg 875 Trp Cys Ile Gly Leu Tyr
 Asn Val Met Phe 885 Thr Ala Met Pro Pro 890 Leu Thr Leu Gly Ile Phe Gly
 Arg Ser Cys 900 Arg Lys Glu Asn Met 905 Leu Lys Tyr Pro Glu Ile Tyr Lys
 Thr Ser Gln Asn Ala Leu Asp 920 Phe Asn Thr Lys Val Phe Trp Val His
 Cys 930 Leu Asn Gly Leu Phe 935 His Ser Val Ile Leu Phe Trp Phe Pro Leu
 945 Lys Ala Leu Gln Tyr 950 Gly Thr Ala Phe Gly Asn Gly Lys Thr Ser Asp
 Tyr Leu Leu Leu 965 Gly Asn Phe Val Tyr Thr Phe Val Val Ile Thr Val
 Cys Leu Lys 980 Ala Gly Leu Glu Thr 985 Ser Tyr Trp Thr Trp Phe Ser His
 Ile Ala 995 Ile Trp Gly Ser Ile 1000 Ala Leu Trp Val Val Phe Phe Gly
 1010 Ile Tyr Ser Ser Leu Trp 1015 Pro Ala Ile Pro Met Ala Pro Asp Met
 1025 Ser Gly Glu Ala Ala Met 1030 Leu Phe Ser Ser Gly Val Phe Trp Met
 1040 Gly Leu Leu Phe Ile Pro 1045 Val Ala Ser Leu Leu Leu Asp Val Val
 Tyr Lys 1055 Val Ile Lys Arg Thr 1060 Ala Phe Lys Thr Leu Val Asp Glu
 Val Gln 1070 Glu Leu Glu Ala Lys 1075 Ser Gln Asp Pro Gly Ala Val Val
 Leu Gly 1085 Lys Ser Leu Thr Glu 1090 Arg Ala Gln Leu Leu Lys Asn Val
 Phe Lys 1100 Lys Asn His Val Asn 1105 Leu Tyr Arg Ser Glu Ser Leu Gln
 1115 Gln Asn Leu Leu His Gly Tyr 1120 Ala Phe Ser Gln Asp Glu Asn Gly
 1130 Ile Val Ser Gln Ser Glu Val 1135 Ile Arg Ala Tyr Asp Thr Thr Lys
 1145 Gln Arg Pro Asp Glu Trp 1150

<210> 177
 <211> 1148
 <212> PRT
 <213> Mouse

<400> 177

Met Ser Arg Ala Thr Ser Val Gly Asp Gln Leu Glu Ala Pro Ala Arg
 1 5 10 15
 Ile Ile Tyr Leu Asn Gln Ser His Leu Asn Lys Phe Cys Asp Asn Arg
 20 25 30
 Ile Ser Thr Ala Lys Tyr Ser Val Leu Thr Phe Leu Pro Arg Phe Leu

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Tyr	Leu	Gln	Ile	Arg	Arg	Ala	Asn	Ala	Phe	Leu	Phe	Ile	Ala
50	Leu	Gln	Gln	Ile	Pro	55	Val	Ser	Pro	60	Gly	Arg	Tyr
65	Leu	Val	Pro	Leu	Val	70	Ile	Ile	Leu	75	Ala	Gly	Ile
80	Leu	Val	Pro	Leu	Val	85	Ile	Ile	Leu	90	Ala	Gly	Ile
95	Ile	Glu	Asp	Phe	100	Lys	Arg	His	Lys	105	Asn	Ala	Val
110	Lys	Thr	Ile	Val	Leu	Arg	Asn	Gly	120	Met	Trp	His	Thr
125	Glu	Val	Ala	Val	Gly	Asp	Ile	Val	Lys	135	Val	Leu	Asn
140	Pro	Ala	Asp	Met	Val	150	Asn	Leu	Asp	155	Glu	Thr	Asn
160	Tyr	Val	Glu	Thr	Ala	165	Asn	Leu	Asp	170	Glu	Thr	Asn
175	Gln	Gly	Leu	Ser	180	His	Thr	Thr	Asp	185	Glu	Thr	Arg
190	Lys	Leu	Ser	Gly	Arg	Ile	Glu	Cys	200	Glu	Gly	Pro	Asn
205	Asp	Phe	Thr	Gly	Asn	Leu	His	215	Leu	Asp	Gly	Lys	Ser
220	Gly	Pro	Asp	Gln	Ile	Leu	230	Leu	Arg	Gly	Thr	Gln	235
240	Trp	Val	Phe	Gly	Val	245	Val	Tyr	Thr	Gly	250	His	Asp
255	Gln	Asn	Ser	Thr	260	Lys	Ala	Pro	Leu	Lys	265	Arg	Ser
270	Thr	Asn	Val	Gln	Ile	Leu	Val	Leu	280	Phe	Gly	Ile	Leu
285	Leu	Val	Ser	Ser	Val	Gly	Ala	295	Leu	Phe	Trp	Asn	Gly
300	Lys	Ser	Trp	Tyr	Ile	Lys	Lys	Met	Asp	Thr	Asn	315	Ser
320	Tyr	Asn	Leu	Leu	Thr	325	Phe	Ile	Ile	Leu	Tyr	330	Asn
335	Ser	Leu	Leu	Val	Thr	Leu	Glu	Val	Val	345	Lys	Tyr	Thr
350	Ile	Asn	Trp	Asp	Met	Asp	Met	Tyr	360	Tyr	Ile	Glu	Asn
365	Met	Ala	Arg	Thr	Ser	Asn	Leu	375	Gly	Thr	Leu	Thr	Cys
380	Leu	Phe	Ser	Asp	Lys	Thr	390	Gly	Thr	Leu	Thr	Cys	395
400	Lys	Lys	Cys	Ser	Ile	405	Ala	Gly	Val	Thr	410	Gly	His
415	Ala	Arg	Glu	Gln	420	Ser	Ser	Asp	Asp	425	Phe	Cys	Arg
430	Asn	Asp	Ser	Cys	Asp	Phe	Asn	Asp	440	Pro	Arg	Leu	Leu
445	Asp	Gln	His	Pro	Thr	Ala	Pro	455	Cys	Ile	Gln	Glu	Phe
460	Ala	Val	Cys	His	Thr	Val	470	Val	Pro	Glu	Lys	Asp	475
480	Tyr	Gln	Ala	Ser	Ser	485	Pro	Asp	Glu	Ala	Ala	490	Leu
495	Lys	Leu	Gly	Phe	Val	Phe	Thr	Gly	Arg	505	Thr	Pro	Tyr
510	Glu	Ala	Met	Gly	Gln	Glu	Gln	Thr	520	Phe	Gly	Ile	Leu
525	Phe	Ser	Ser	Asp	Arg	Lys	Arg	535	Met	Ser	Val	Ile	Val

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Gly Gln Leu Arg Leu Tyr Cys Lys Gly Ala Asp Asn Val Ile Phe Glu
 545 Arg Leu Ser Lys Asp 550 Ser Lys Tyr Met Glu 555 Thr Leu Cys His 560
 Glu Tyr Phe Ala Thr 565 Glu Gly Leu Arg 570 Thr Leu Cys Val Ala Tyr Ala
 580 Asp Leu Ser 585 Glu Asn Glu Tyr Glu 590 Trp Leu Lys Val 595 Gln Glu
 Ala Ser Ile Ile Leu Lys Asp 600 Arg Ala Gln Arg Leu 605 Glu Cys Tyr
 610 Glu Ile Ile Glu Lys Asn 615 Leu Leu Leu Gly 620 Ala Thr Ala Ile Glu
 625 Asp Arg Leu Gln Ala 630 Gly Val Pro Glu Thr 635 Ile Ala Thr Leu 640
 Ala Glu Ile Lys 645 Ile Trp Val Leu Thr 650 Gly Asp Lys Gln Glu 655
 Ile Asn Ile Gly Tyr Ser Cys Arg 660 Leu Val Ser Gln Asn 665 Met Ala Leu
 Ile Leu Leu Lys Glu Asp Ser 670 Leu Asp Ala Thr Arg 675 Ala Ile Thr
 Gln His Cys Thr Asp Leu Gly Asn Leu Leu 680 Tyr 685 Lys Glu Asn Asp Val
 705 Ala Leu Ile Ile Asp 710 Gly His Thr Leu Lys 715 Tyr Ala Leu Ser Phe 720
 Val Arg Arg Ser Phe Leu Asp Leu Ala 725 Lys Ser Cys Lys Ala Val Ile
 Cys Cys Arg Val Ser Pro Leu Gln Lys Ser Glu Ile Val 730 Asp Val Val
 740 Lys Lys Arg Val Lys Ala Ile Thr Leu Ala Ile Gly 745 Asp Gly Ala Asn
 755 Asp Val Gly Met Ile Gln Thr Ala His Val Gly 760 Val Gly Ile Ser Gly
 770 Asn Glu Gly Met Gln 775 Ala Thr Asn Asn Ser 780 Asp Tyr Ala Ile Ala Gln
 785 Phe Ser Tyr Leu 790 Glu Lys Leu Leu 800 Val His Gly Ala Trp Ser Tyr
 Asn Arg Val Thr Lys Cys Ile Leu 810 Tyr Cys Phe Tyr Lys 815 Asn Val Val
 Leu Tyr Ile Ile Glu Leu Trp Phe Ala Phe Val Asn 820 Gly Phe Ser Gly
 835 Gln Ile Leu Phe Glu Arg 840 Trp Cys Ile Gly Leu Tyr Asn Val Ile Phe
 855 Thr Ala Leu Pro Pro 860 Phe Thr Leu Gly Ile Phe Glu Arg Ser Cys Thr
 865 Gln Glu Ser Met Leu Arg Phe Pro Gln 870 Leu Tyr Arg Ile Thr Gln Asn
 885 Ala Glu Gly Phe Asn Thr Lys Val Phe Trp Gly His Cys 890 Ile Asn Ala
 900 Leu Val His Ser Leu Ile Leu Phe Trp Val Pro Met 910 Lys Ala Leu Glu
 915 His Asp Thr Pro Val Thr Ser Gly His Ala Thr 920 Asp Tyr Leu Phe Val
 930 Gly Asn Ile Val Tyr Thr Tyr Val Val Val Thr Val Cys Leu Lys 935 Ala
 945 Gly Leu Glu Thr Thr Ala Trp Thr Lys 950 Phe Ser His Leu Ala Val Trp
 965 Gly Ser Met Leu Ile Trp Leu Val Phe Phe Gly Val Tyr 970 Ser Thr Ile
 980 Trp Pro Thr Ile Pro Ile Ala 985 Pro Asp Met Lys Gly Gln Ala Thr
 995 Met Val Leu Ser Ser Ala Tyr 1000 Phe Trp Leu Gly Leu Phe Leu Val
 1010 Pro Thr Ala Cys Leu Ile Glu Asp Val Ala Trp Arg Ala Ala Lys

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1040	1045	1050
His Thr Cys Lys Lys Thr	Leu Leu Glu Glu Val	Gln Glu Leu Glu
1055	1060	1065
Thr Lys Ser Arg Val Met	Gly Lys Ala Met Leu	Arg Asp Ser Asn
1070	1075	1080
Gly Lys Arg Met Asn Glu	Arg Asp Arg Leu Ile	Lys Arg Leu Ser
1085	1090	1095
Arg Lys Thr Pro Pro Thr	Leu Phe Arg Thr Gly	Ser Ile Gln Gln
1100	1105	1110
Cys Val Ser His Gly Tyr	Ala Phe Ser Gln Glu	Glu His Gly Ala
1115	1120	1125
Val Thr Gln Glu Glu Ile	Val Arg Ala Tyr Asp	Thr Thr Lys Glu
1130	1135	1140
Asn Ser Arg Lys Lys		
1145		

<210> 178
 <211> 839
 <212> PRT
 <213> Human

<400> 178

Met Lys Lys Trp Ser Ser Thr Asp Leu Gly Ala Ala Ala Asp Pro Leu	1	5	10	15
Gln Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Ser Arg	20	25	30	
Pro Pro Pro Ala Lys Pro Gln Leu Ser Thr Ala Lys Ser Arg Thr Arg	35	40	45	
Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro	50	55	60	
His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro	65	70	75	80
Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu	85	90	95	
Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu	100	105	110	
Tyr Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Cys Gln	115	120	125	
Asp Leu Glu Ser Leu Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu	130	135	140	
Thr Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu	145	150	155	160
Lys Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu	165	170	175	
Leu Leu Glu Ile Ala Arg Gln Thr Asp Ser Leu Lys Glu Leu Val Asn	180	185	190	
Ala Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile	195	200	205	
Ala Ile Glu Arg Arg Asn Met Ala Leu Val Thr Leu Leu Val Glu Asn	210	215	220	
Gly Ala Asp Val Gln Ala Ala His Gly Asp Phe Phe Lys Lys Thr	225	230	235	240
Lys Gly Arg Pro Gly Phe Tyr Phe Gly Glu Leu Pro Leu Ser Leu Ala	245	250	255	
Ala Cys Thr Asn Gln Leu Gly Ile Val Lys Phe Leu Leu Gln Asn Ser	260	265	270	
Trp Gln Thr Ala Asp Ile Ser Ala Arg Asp Ser Val Gly Asn Thr Val	275	280	285	
Leu His Ala Leu Val Glu Val Ala Asp Asn Thr Ala Asp Asn Thr Lys	290	295	300	
Phe Val Thr Ser Met Tyr Asn Glu Ile Leu Met Leu Gly Ala Lys Leu	305	310	315	320

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His Pro Thr Leu Lys³²⁵ Leu Glu Glu Leu Thr³³⁰ Asn Lys Lys Gly Met³³⁵ Thr
 Pro Leu Ala Leu³⁴⁰ Ala Ala Gly Thr Gly³⁴⁵ Lys Ile Gly Val Leu³⁵⁰ Ala Tyr
 Ile Leu Gln Arg Glu Ile Gln Glu³⁶⁰ Pro Glu Cys Arg His³⁶⁵ Ser Leu Tyr Asp
 Lys Phe³⁷⁰ Thr Glu Trp Ala Tyr³⁷⁵ Gly Pro Val His Ser³⁸⁰ Val Leu Tyr Asp
 Leu Ser Cys Ile Asp Thr³⁹⁰ Cys Glu Lys Asn Ser³⁹⁵ Leu Glu Val Ile⁴⁰⁰
 Ala Tyr Ser Ser Ser⁴⁰⁵ Glu Thr Pro Asn Arg His⁴¹⁰ Asp Met Leu⁴¹⁵ Val
 Glu Pro Leu Asn Arg Leu Leu Gln Asp⁴²⁵ Lys Trp Asp Arg Phe⁴³⁰ Val Lys
 Arg Ile Phe⁴³⁵ Tyr Phe Asn Phe Leu⁴⁴⁰ Val Tyr Cys Leu Tyr⁴⁴⁵ Ile Ile
 Phe Thr Met Ala Ala Tyr Tyr⁴⁵⁵ Arg Pro Val Asp Gly⁴⁶⁰ Thr Pro Pro Phe
 Lys Met Glu Lys Thr Gly⁴⁷⁰ Asp Tyr Phe Arg Val⁴⁷⁵ Gly Ile Gln Tyr⁴⁸⁰
 Ser Val Leu Gly Gly⁴⁸⁵ Val Tyr Phe Phe Phe⁴⁹⁰ Arg Gly Ile Gln Tyr⁴⁹⁵ Phe
 Leu Gln Arg Arg⁵⁰⁰ Pro Ser Met Lys Thr⁵⁰⁵ Leu Phe Val Asp Ser⁵¹⁰ Ser
 Glu Met Leu Phe Phe Leu Gln Ser⁵²⁰ Phe Met Leu Ala⁵²⁵ Thr Val Val
 Leu Tyr Phe Ser His Leu Lys⁵³⁵ Glu Tyr Val Ala Ser⁵⁴⁰ Met Val Phe Ser
 Leu Ala Leu Gly Trp Thr⁵⁵⁰ Asn Met Leu Tyr Tyr⁵⁵⁵ Thr Arg Gly Phe Gln⁵⁶⁰
 Gln Met Gly Ile Tyr⁵⁶⁵ Ala Val Met Ile Glu⁵⁷⁰ Lys Met Ile Leu Arg Asp⁵⁷⁵
 Leu Cys Arg Phe Met Phe Val Tyr Ile⁵⁸⁵ Val Phe Leu Phe Gly⁵⁹⁰ Phe Ser
 Thr Ala Val Val Thr Leu Ile Glu⁶⁰⁰ Asp Gly Lys Asn Asp⁶⁰⁵ Ser Leu Pro
 Ser Glu Ser Thr Ser His Arg⁶¹⁵ Trp Arg Gly Pro Ala⁶²⁰ Cys Arg Pro Pro
 Asp Ser Ser Tyr Asn Ser⁶³⁰ Leu Tyr Ser Thr Cys⁶³⁵ Leu Glu Leu Phe Lys⁶⁴⁰
 Phe Thr Ile Gly Met⁶⁴⁵ Gly Asp Leu Glu Phe⁶⁵⁰ Thr Glu Asn Tyr Asp⁶⁵⁵ Phe
 Lys Ala Val Phe⁶⁶⁰ Ile Ile Leu Leu Leu⁶⁶⁵ Ala Tyr Val Ile Leu Thr Tyr
 Ile Leu Leu Leu Asn Met Leu Ile⁶⁸⁰ Ala Leu Met Gly Glu⁶⁸⁵ Thr Val Asn
 Lys Ile Ala Gln Glu Ser Lys⁶⁹⁵ Asn Ile Trp Lys Leu⁷⁰⁰ Gln Arg Ala Ile
 Thr Ile Leu Asp Thr Glu⁷¹⁰ Lys Ser Phe Leu Lys⁷¹⁵ Cys Met Arg Lys Ala⁷²⁰
 Phe Arg Ser Gly Lys⁷²⁵ Leu Leu Gln Val Gly⁷³⁰ Tyr Thr Pro Asp Gly⁷³⁵ Lys
 Asp Asp Tyr Arg Trp Cys Phe Arg Val⁷⁴⁵ Asp Glu Val Asn Trp Thr Thr
 Trp Asn Thr Asn Val Gly Ile Ile⁷⁶⁰ Asn Glu Asp Pro Gly⁷⁶⁵ Asn Cys Glu
 Gly Val Lys Arg Thr Leu Ser⁷⁷⁵ Phe Ser Leu Arg Ser⁷⁸⁰ Ser Arg Val Ser
 Gly Arg His Trp Lys Asn⁷⁹⁰ Phe Ala Leu Val Pro⁷⁹⁵ Leu Leu Arg Glu Ala⁸⁰⁰
 Ser Ala Arg Asp Arg Gln Ser Ala Gln Pro⁸¹⁰ Glu Glu Val Tyr Leu Arg
 Gln Phe Ser Gly Ser Leu Lys Pro Glu Asp Ala Glu Val Phe Lys Ser

Pro Ala Ala 820 Ser Gly Glu Lys 830